The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/686,490C_

Source: _1FWD_

Date Processed by STIC: _2/25/05_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER</u> <u>VERSION 4.2.2 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**
   U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: /0/686,490C

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics
Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

·2 ____ Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino Numbering — The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ____ Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length — Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ____ Skipped Sequences (OLD RULES) — Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____ Skipped Sequences (NEW RULES) — Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____ Invalid <213> Response — Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ____ Use of <220> — Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n/Xaa — "n" can only represent a single <u>nucleotide</u>; "Xaa" can only represent a single <u>amino acid</u>

AMC – Biotechnology Systems Branch – 09/09/2003

IFWO

RAW SEQUENCE LISTING   DATE: 02/25/2005
PATENT APPLICATION: US/10/686,490C TIME: 10:06:06

   Input Set : A:\PTO.SR.txt
   Output Set: N:\CRF4\02252005\J686490C.raw

```
   3 <110> APPLICANT: Bayer Aktiengesellschaft
   4 <120> TITLE OF INVENTION: Anti-Kazlauskas-Lipases
   5 <130> FILE REFERENCE: LeA 35 991
C-->  6 <140> CURRENT APPLICATION NUMBER: US/10/686,490C
C-->  6 <141> CURRENT FILING DATE: 2003-10-15
   6 <160> NUMBER OF SEQ ID NOS: 2
   7 <170> SOFTWARE: PatentIn version 3.1
   9 <210> SEQ ID NO: 1
  10 <211> LENGTH: 885
  11 <212> TYPE: DNA
  12 <213> ORGANISM: unknown
  13 <220> FEATURE:
  14 <221> NAME/KEY: CDS
  15 <222> LOCATION: (1)..(885)
  16 <223> OTHER INFORMATION: bacterial
  18 <400> SEQUENCE: 1
  19 atg gca cag gtg aag gcc aac ggc att acc ctc gag tat gaa gag cag        48
  20 Met Ala Gln Val Lys Ala Asn Gly Ile Thr Leu Glu Tyr Glu Glu Gln
  21 1               5                   10                  15
  23 ggc cat cgc cac cat ccg tcc atg ctc ctc att atg ggc ctg ggc ggc        96
  24 Gly His Arg His His Pro Ser Met Leu Leu Ile Met Gly Leu Gly Gly
  25              20                  25                  30
  27 cag tta atc gac tgg ccc gag gag ttc atc cgg ggg ctg gct gaa cga       144
  28 Gln Leu Ile Asp Trp Pro Glu Glu Phe Ile Arg Gly Leu Ala Glu Arg
  29          35                  40                  45
  31 ggc ttc cgg gta atc tgt ttc gac aac cgc gac gcg ggg ctt tcg acg       192
  32 Gly Phe Arg Val Ile Cys Phe Asp Asn Arg Asp Ala Gly Leu Ser Thr
  33      50                  55                  60
  35 aaa ctt gaa ggc gtg aaa aaa ccg aac att gcc cgg gta ttt ctc ctg       240
  36 Lys Leu Glu Gly Val Lys Lys Pro Asn Ile Ala Arg Val Phe Leu Leu
  37 65                  70                  75                  80
  39 gcg agc atg ggc cta aag ccc agg gtg cct tac acc ctc gac gac atg       288
  40 Ala Ser Met Gly Leu Lys Pro Arg Val Pro Tyr Thr Leu Asp Asp Met
  41                  85                  90                  95
  43 gcc ctg gac acc gtg ggg ctg atg gat gcc ctg ggc att gag agc acc       336
  44 Ala Leu Asp Thr Val Gly Leu Met Asp Ala Leu Gly Ile Glu Ser Thr
  45              100                 105                 110
  47 cac gta gtt ggc gtc tcc atg ggc ggc atg att gcg cag att cta ggg       384
  48 His Val Val Gly Val Ser Met Gly Gly Met Ile Ala Gln Ile Leu Gly
  49              115                 120                 125
  51 gcg aag cac ggg gag cgg gtg aaa tcc ctt acc ctg atg att acc tcc       432
  52 Ala Lys His Gly Glu Arg Val Lys Ser Leu Thr Leu Met Ile Thr Ser
  53      130                 135                 140
```

RAW SEQUENCE LISTING   DATE: 02/25/2005
PATENT APPLICATION: US/10/686,490C   TIME: 10:06:06

Input Set : A:\PTO.SR.txt
Output Set: N:\CRF4\02252005\J686490C.raw

```
55 tcc ggc aac ccc cgc atg ccg gcg ccc agg ccg cag gtg ctg caa aag    480
56 Ser Gly Asn Pro Arg Met Pro Ala Pro Arg Pro Gln Val Leu Gln Lys
57 145             150             155             160
59 ttt atg cgg gtg ccc aag agc atg gat aag gaa gag tgg att aaa tac    528
60 Phe Met Arg Val Pro Lys Ser Met Asp Lys Glu Glu Trp Ile Lys Tyr
61             165             170             175
63 aac ttg gag ctt tta acc acc atc ggc agc ccc ggg ttg gac cgg gag    576
64 Asn Leu Glu Leu Leu Thr Thr Ile Gly Ser Pro Gly Leu Asp Arg Glu
65             180             185             190
67 aag ctg gcc tta gac gtg agg aag agc ata gag cgg tgc ctt tgc ccc    624
68 Lys Leu Ala Leu Asp Val Arg Lys Ser Ile Glu Arg Cys Leu Cys Pro
69             195             200             205
71 gaa ggc acg cag cgg cag ctg gca gcc atc ctg cag agc ggc agc agg    672
72 Glu Gly Thr Gln Arg Gln Leu Ala Ala Ile Leu Gln Ser Gly Ser Arg
73     210             215             220
75 gtg aag ctg ctc cgg cgg atc gct gtc ccc acc ctg gtc atc agc ggg    720
76 Val Lys Leu Leu Arg Arg Ile Ala Val Pro Thr Leu Val Ile Ser Gly
77 225             230             235             240
79 gcg gaa gat ccc ctc ctg ccg tac cag tgc ggc cgg gac att gcc gac    768
80 Ala Glu Asp Pro Leu Leu Pro Tyr Gln Cys Gly Arg Asp Ile Ala Asp
81             245             250             255
83 cat atc ccg gga gcc cgc ttc gag ctc atc gag ggc atg ggg cac gac    816
84 His Ile Pro Gly Ala Arg Phe Glu Leu Ile Glu Gly Met Gly His Asp
85             260             265             270
87 att ccc gag cgg cac atc ccc cgg ctg att gag ctc atc gcc ggg cac    864
88 Ile Pro Glu Arg His Ile Pro Arg Leu Ile Glu Leu Ile Ala Gly His
89             275             280             285
91 gcc gcg gcc gcg gaa gct taa                                        885
92 Ala Ala Ala Ala Glu Ala
93     290
96 <210> SEQ ID NO: 2
97 <211> LENGTH: 294
98 <212> TYPE: PRT
99 <213> ORGANISM: unknown
```

W--> 102 <220> FEATURE:
W--> 102 <223> OTHER INFORMATION:
W--> 102 <400> 2

```
104 Met Ala Gln Val Lys Ala Asn Gly Ile Thr Leu Glu Tyr Glu Glu Gln
105 1             5             10             15
108 Gly His Arg His His Pro Ser Met Leu Leu Ile Met Gly Leu Gly Gly
109             20             25             30
112 Gln Leu Ile Asp Trp Pro Glu Glu Phe Ile Arg Gly Leu Ala Glu Arg
113     35             40             45
116 Gly Phe Arg Val Ile Cys Phe Asp Asn Arg Asp Ala Gly Leu Ser Thr
117 50             55             60
120 Lys Leu Glu Gly Val Lys Lys Pro Asn Ile Ala Arg Val Phe Leu Leu
121 65             70             75             80
124 Ala Ser Met Gly Leu Lys Pro Arg Val Pro Tyr Thr Leu Asp Asp Met
125             85             90             95
```

RAW SEQUENCE LISTING   DATE: 02/25/2005
PATENT APPLICATION: US/10/686,490C   TIME: 10:06:06

Input Set : A:\PTO.SR.txt
Output Set: N:\CRF4\02252005\J686490C.raw

```
128 Ala Leu Asp Thr Val Gly Leu Met Asp Ala Leu Gly Ile Glu Ser Thr
129         100                 105                 110
132 His Val Val Gly Val Ser Met Gly Gly Met Ile Ala Gln Ile Leu Gly
133     115                 120                 125
136 Ala Lys His Gly Glu Arg Val Lys Ser Leu Thr Leu Met Ile Thr Ser
137     130                 135                 140
140 Ser Gly Asn Pro Arg Met Pro Ala Pro Arg Pro Gln Val Leu Gln Lys
141 145                 150                 155                 160
144 Phe Met Arg Val Pro Lys Ser Met Asp Lys Glu Glu Trp Ile Lys Tyr
145                 165                 170                 175
148 Asn Leu Glu Leu Leu Thr Thr Ile Gly Ser Pro Gly Leu Asp Arg Glu
149         180                 185                 190
152 Lys Leu Ala Leu Asp Val Arg Lys Ser Ile Glu Arg Cys Leu Cys Pro
153         195                 200                 205
156 Glu Gly Thr Gln Arg Gln Leu Ala Ala Ile Leu Gln Ser Gly Ser Arg
157     210                 215                 220
160 Val Lys Leu Leu Arg Arg Ile Ala Val Pro Thr Leu Val Ile Ser Gly
161 225                 230                 235                 240
164 Ala Glu Asp Pro Leu Leu Pro Tyr Gln Cys Gly Arg Asp Ile Ala Asp
165                 245                 250                 255
168 His Ile Pro Gly Ala Arg Phe Glu Leu Ile Glu Gly Met Gly His Asp
169                 260                 265                 270
172 Ile Pro Glu Arg His Ile Pro Arg Leu Ile Glu Leu Ile Ala Gly His
173     275                 280                 285
176 Ala Ala Ala Ala Glu Ala
177     290
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 02/25/2005
PATENT APPLICATION: US/10/686,490C   TIME: 10:06:07

Input Set : A:\PTO.SR.txt
Output Set: N:\CRF4\02252005\J686490C.raw

error explanation

Use of <220> Feature(NEW RULES):
Sequence(s)__are missing the <220> Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence"
or"Unknown". Please explain source of genetic material in <220> to <223>
section (See "Federal Register," 6/01/98, Vol. 63, No. 104,pp.29631-32)
(Sec.1.823 of new Rules)

Seq#:2

VERIFICATION SUMMARY   DATE: 02/25/2005
PATENT APPLICATION: **US/10/686,490C**   TIME: 10:06:07

Input Set : **A:\PTO.SR.txt**
Output Set: **N:\CRF4\02252005\J686490C.raw**

L:6 M:270 C: Current Application Number differs, Replaced Current Application No
L:6 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:102 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:2, <213>
ORGANISM:unknown
L:102 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:2, <213>
ORGANISM:unknown
L:102 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:102